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S-65 Domestication: human-induced evolution

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Level 3

The road to sorghum domestication: evidence from nucleotide diversity and gene expression patterns

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AIMS:

Sorghum bicolor is the fifth cereal worldwide for grain production, constituting the staple food for around 500 million people. The release of its genome sequence, its phylogenetic proximity with other important C4 species (maize, switchgrass, sugarcane) and its low genome complexity contribute to its interest on a more fundamental level. Sorghum bicolor wild relatives (ssp. verticilliflorum) and domesticated (ssp. bicolor) pools are inter-fertile and intense gene flow occurs. However, a clear domestication syndrome is visible (plant architecture, shattering, dormancy and seed weight). In spite of its agronomical importance, the evolutionary dynamics of sorghum domestication and the genetic bases of adaptations to natural and anthropogenic pressures are not well understood. Here we leverage transcriptomic and genomic resources to improve our knowledge on the evolutionary history of S. bicolor, with a particular focus on the consequences of the domestication process. As a first step, gene expression and nucleotide variability of the expressed genes were analyzed in 11 cultivated and 9 wild accessions selected to maximize the genetic coverage of these two pools. The cultivated compartment harbors 30% lower genetic diversity than the wild pool, which supports the occurrence of a genetic bottleneck in the domestication history of sorghum. More than 900 genes are significantly differentially expressed between the two compartments. Among them, genes involved in photosynthesis and in reduction-oxidation processing of seed storage proteins are over-represented. Further analyses revealed that domestication reduced significantly the variability of the isoform expression balance (expression ratio of the alternative proteins coded by a single gene) in cultivated sorghum. Scans for local adaptation and positive selection on large cultivated and wild panels genotyped with genotyping by sequencing approaches are ongoing. Overall, these analyses pave the way towards the identification of key domestication genes that could be useful for conservation strategies but also for breeding purposes.